STIC Biotechnology Systems Branch

RAW SEQUENCE LISTING
ERROR REPORT

The Biotechnology Systems Branch of the Scientific and Technical Information
Center (STIC) detected errors when processing the following computer readable
form:

Application Serial Number: _10/563,503A_
Source: _1Rxo_
Date Processed by STIC: _6/14/06_

THE ATTACHED PRINTOUT EXPLAINS DETECTED ERRORS.
PLEASE FORWARD THIS INFORMATION TO THE APPLICANT BY EITHER:
1) INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE
   APPLICANT, WITH A NOTICE TO COMPLY or,
2) TELEPHONING APPLICANT AND FAXING A COPY OF THIS PRINTOUT, WITH A
   NOTICE TO COMPLY
FOR CRF SUBMISSION AND PATENTIN SOFTWARE QUESTIONS, PLEASE CONTACT
MARK SPENCER, TELEPHONE: 571-272-2510; FAX: 571-273-0221

TO REDUCE ERRORED SEQUENCE LISTINGS, PLEASE USE THE **CHECKER**
VERSION 4.4.0 PROGRAM, ACCESSIBLE THROUGH THE U.S. PATENT AND
TRADEMARK OFFICE WEBSITE. SEE BELOW FOR ADDRESS:
        http://www.uspto.gov/web/offices/pac/checker/chkrnote.htm

Applicants submitting genetic sequence information electronically on diskette or CD-Rom should be aware that there is
a possibility that the disk/CD-Rom may have been affected by treatment given to all incoming mail.
Please consider using alternate methods of submission for the disk/CD-Rom or replacement disk/CD-Rom.
Any reply including a sequence listing in electronic form should NOT be sent to the 20231 zip code address for the
United States Patent and Trademark Office, and instead should be sent via the following to the indicated addresses:

1. EFS-Bio (<http://www.uspto.gov/ebc/efs/downloads/documents.htm> , EFS Submission
   User Manual - ePAVE)
2. U.S. Postal Service: Commissioner for Patents, P.O. Box 1450, Alexandria, VA 22313-1450
3. Hand Carry, Federal Express, United Parcel Service, or other delivery service (EFFECTIVE 01/14/05):
   U.S. Patent and Trademark Office, Mail Stop Sequence, Customer Window, Randolph Building, 401 Dulany Street,
   Alexandria, VA 22314

Revised 01/10/06

Raw Sequence Listing Error Summary

ERROR DETECTED   **SUGGESTED CORRECTION**   SERIAL NUMBER: _10/563, 503A_

ATTN: NEW RULES CASES: PLEASE DISREGARD ENGLISH "ALPHA" HEADERS, WHICH WERE INSERTED BY PTO SOFTWARE

1 ____ Wrapped Nucleics   The number/text at the end of each line "wrapped" down to the next line. This may occur if your file
    Wrapped Aminos   was retrieved in a word processor after creating it. Please adjust your right margin to .3; this will
    prevent "wrapping."

2 ____ Invalid Line Length   The rules require that a line not exceed 72 characters in length. This includes white spaces.

3 ____ Misaligned Amino   The numbering under each 5th amino acid is misaligned. Do not use tab codes between numbers;
    Numbering   use space characters, instead.

4 ____ Non-ASCII   The submitted file was not saved in ASCII(DOS) text, as required by the Sequence Rules. Please
    ensure your subsequent submission is saved in ASCII text.

5 ____ Variable Length   Sequence(s) ____ contain n's or Xaa's representing more than one residue. Per Sequence Rules,
    each n or Xaa can only represent a single residue. Please present the maximum number of each
    residue having variable length and indicate in the <220>-<223> section that some may be missing.

6 ____ PatentIn 2.0   A "bug" in PatentIn version 2.0 has caused the <220>-<223> section to be missing from amino acid
    "bug"   sequences(s) _____. Normally, PatentIn would automatically generate this section from the
    previously coded nucleic acid sequence. Please manually copy the relevant <220>-<223> section to
    the subsequent amino acid sequence. **This applies to the mandatory <220>-<223> sections for**
    Artificial or Unknown sequences.

7 ____ Skipped Sequences   Sequence(s) ____ missing. If intentional, please insert the following lines for each skipped sequence:
    (OLD RULES)   (2) INFORMATION FOR SEQ ID NO:X: (insert SEQ ID NO where "X" is shown)
    (i)   SEQUENCE CHARACTERISTICS: (Do not insert any subheadings under this heading)
    (xi) SEQUENCE DESCRIPTION:SEQ ID NO:X: (insert SEQ ID NO where "X" is shown)
    This sequence is intentionally skipped
    Please also adjust the "(ii) NUMBER OF SEQUENCES:" response to include the skipped sequences.

8 ____ Skipped Sequences   Sequence(s) ____ missing. If intentional, please insert the following lines for each skipped sequence.
    (NEW RULES)   <210> sequence id number
    <400> sequence id number
    000

9 ____ Use of n's or Xaa's   Use of n's and/or Xaa's have been detected in the Sequence Listing.
    (NEW RULES)   Per 1.823 of Sequence Rules, use of <220>-<223> is MANDATORY if n's or Xaa's are present.
    In <220> to <223> section, please explain location of n or Xaa, and which residue n or Xaa represents.

10 ____ Invalid <213>   Per 1.823 of Sequence Rules, the only valid <213> responses are: Unknown, Artificial Sequence, or
    Response   scientific name (Genus/species). <220>-<223> section is **required** when <213> response is Unknown or
    is Artificial Sequence. (see item 11 below)

11 ____ Use of <220>   Sequence(s) ____ missing the <220> "Feature" and associated numeric identifiers and responses. Use
    of <220> to <223> is MANDATORY if <213> "Organism" response is "Artificial Sequence" or "Unknown."
    Please explain source of genetic material in <220> to <223> section or use "chemically synthesized" as
    explanation. (See "Federal Register," 06/01/1998, Vol. 63, No. 104, pp. 29631-32), also Sec. 1.823 of
    Sequence Rules

12 ____ PatentIn 2.0   Please do not use "Copy to Disk" function of PatentIn version 2.0. This causes a corrupted file,
    "bug"   resulting in missing mandatory numeric identifiers and responses (as indicated on raw sequence
    listing). Instead, please use "File Manager" or any other manual means to copy file to floppy disk.

13 ____ Misuse of n/Xaa   "n" can only represent a single <u>nucleotide</u>; "Xaa" can only represent a single <u>amino acid</u>

AMC – STIC Systems Branch – 03/02/06

IFWO

RAW SEQUENCE LISTING
PATENT APPLICATION: US/10/563,503A

DATE: 06/14/2006
TIME: 09:50:11   *see item 2*
on Error summary
sheet

Input Set : A:\PTO.RJ.txt
Output Set: N:\CRF4\06142006\J563503A.raw

Does Not Comply
Corrected Diskette Needed

```
   5 <110> APPLICANT: Stordeur, Patrick
   6         Goldman, Michel
  10 <120> TITLE OF INVENTION: Device, kit and method for pulsing biological samples with
an agent and
  11         stabilising the sample so pulsed
  15 <130> FILE REFERENCE: DECLE35.005APC
  19 <140> CURRENT APPLICATION NUMBER: 10/563,503A
  20 <141> CURRENT FILING DATE: 2006-01-04
  22 <150> PRIOR APPLICATION NUMBER: PCT/EP03/07453
  23 <151> PRIOR FILING DATE: 2003-07-10
  26 <160> NUMBER OF SEQ ID NOS: 10
  28 <170> SOFTWARE: PatentIn version 3.1
  32 <210> SEQ ID NO: 1
  34 <211> LENGTH: 22
  36 <212> TYPE: DNA
  38 <213> ORGANISM: Homo sapiens
  42 <400> SEQUENCE: 1
  43 ctcaccagga tgctcacatt ta
  44 <210> SEQ ID NO: 2
  46 <211> LENGTH: 24
  48 <212> TYPE: DNA
  50 <213> ORGANISM: Homo sapiens
  54 <400> SEQUENCE: 2
  55 tccagaggtt tgagttcttc ttct
  56 <210> SEQ ID NO: 3
  58 <211> LENGTH: 25
  60 <212> TYPE: DNA
  62 <213> ORGANISM: Homo sapiens
  66 <220> FEATURE:
  68 <221> NAME/KEY: misc_feature
  70 <222> LOCATION: (1)..(1)
  72 <223> OTHER INFORMATION: N = 6Fam
  75 <220> FEATURE:
  77 <221> NAME/KEY: misc_feature
  79 <222> LOCATION: (25)..(25)
  81 <223> OTHER INFORMATION: N = Tamra-p
  84 <400> SEQUENCE: 3
W--> 85 ntgcccaaga aggccacaga actgn
  86 <210> SEQ ID NO: 4
  88 <211> LENGTH: 21
  90 <212> TYPE: DNA
  92 <213> ORGANISM: Homo sapiens
  96 <400> SEQUENCE: 4
  97 actttgaaca gcctcacaga g
```

22

24

③ "n" *can only represent a nucleotide,*
not a label or
dye.

25

21

RAW SEQUENCE LISTING   DATE: 06/14/2006
PATENT APPLICATION: US/10/563,503A   TIME: 09:50:11

Input Set : **A:\PTO.RJ.txt**
Output Set: **N:\CRF4\06142006\J563503A.raw**

```
 98 <210> SEQ ID NO: 5
100 <211> LENGTH: 20
102 <212> TYPE: DNA
104 <213> ORGANISM: Homo sapiens
108 <400> SEQUENCE: 5
109 ttggaggcag caaagatgtc                                        20
110 <210> SEQ ID NO: 6
112 <211> LENGTH: 23
114 <212> TYPE: DNA
116 <213> ORGANISM: Homo sapiens
120 <220> FEATURE:
122 <221> NAME/KEY: misc_feature
124 <222> LOCATION: (1)..(1)
126 <223> OTHER INFORMATION: N - 6Fam
129 <220> FEATURE:
131 <221> NAME/KEY: misc_feature
133 <222> LOCATION: (23)..(23)
135 <223> OTHER INFORMATION: N = Tamra-p
138 <400> SEQUENCE: 6
139 nctgtgcacc gagttgaccg tan                                    23
140 <210> SEQ ID NO: 7
142 <211> LENGTH: 22
144 <212> TYPE: DNA
146 <213> ORGANISM: Homo sapiens
150 <400> SEQUENCE: 7
151 tgtcacaaac agtgcaccta ct                                     22
152 <210> SEQ ID NO: 8
154 <211> LENGTH: 26
156 <212> TYPE: DNA
158 <213> ORGANISM: Homo sapiens
162 <400> SEQUENCE: 8
163 agttacaata ggtagcaaac cataca                                 26
164 <210> SEQ ID NO: 9
166 <211> LENGTH: 21
168 <212> TYPE: DNA
170 <213> ORGANISM: Homo sapiens
174 <400> SEQUENCE: 9
175 taattgcctc acattgtcac t                                      21
176 <210> SEQ ID NO: 10
178 <211> LENGTH: 21
180 <212> TYPE: DNA
182 <213> ORGANISM: Homo sapiens
186 <400> SEQUENCE: 10
187 attcagctcg aacactttga a                                      21
```

W--> (at line 139)

(handwritten) ⑥

(handwritten) same error as p. 1

RAW SEQUENCE LISTING ERROR SUMMARY   DATE: 06/14/2006
PATENT APPLICATION: US/10/563,503A   TIME: 09:50:12

Input Set : **A:\PTO.RJ.txt**
Output Set: **N:\CRF4\06142006\J563503A.raw**

Please Note:
Use of n and/or Xaa have been detected in the Sequence Listing. Please review the
Sequence Listing to ensure that a corresponding explanation is presented in the <220>
to <223> fields of each sequence which presents at least one n or Xaa.

Seq#:3; N Pos. 1,25
Seq#:6; N Pos. 1,23

VERIFICATION SUMMARY
PATENT APPLICATION: US/10/563,503A

DATE: 06/14/2006
TIME: 09:50:12

Input Set : **A:\PTO.RJ.txt**
Output Set: **N:\CRF4\06142006\J563503A.raw**

L:85 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:3 after pos.:0
L:139 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:6 after pos.:0

GENERAL INFORMATION SECTION

```
            5,<110>  Stordeur, Patrick
            6,       Goldman, Michel
           10,<120>  Device, kit and method for pulsing biological
samples with an agent and stabilising the sample so pulsed
           14,<130>  DECLE35.005APC
           18,<140>  10/563,503
           19,<141>  2006-01-04
           21,<150>  PCT/EP03/07453
           22,<151>  2003-07-10
           25,<160>  10
           27,<170>  PatentIn version 3.1
```

ERRORED LINES SECTION

```
W-->       84 ntgcccaaga aggccacaga actgn
25
W-->      138 nctgtgcacc gagttgaccg tan
23
```

STATISTICS SUMMARY

```
        Application Serial Number: 10/563,503
         Alpha or Numeric or Xml: Numeric
               Application Class:
            Application File Date: 2006-01-04
                        Art Unit:
            Software Application: PatentIN3.1
        Total Number of Sequences: 10
               Total Nucleotides: 225
               Total Amino Acids: 0
               Number of Errors: 0
              Number of Warnings: 2
            Number of Corrections: 0
```